

# SEQUENCE LISTING

<110> Cahoon, Edgar B.  
Cahoon, Rebecca E.

<120> Enzymes Involved In Petroselinic Acid Biosynthesis

<130> BB1413 US NA

<140>  
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<150> 60/169,968  
<151> 9 DECEMBER 1999

<160> 12

<170> Microsoft Office 97

<210> 1  
<211> 1344  
<212> DNA  
<213> Hedera helix

<220>  
<221> unsure  
<222> (997)

<400> 1

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gataatctca	aaagtccgcc	aaatcttcaa	gtcactcact	ctatgccacc	ccaaaagcta	240
gaaatattca	agtccttga	tgattgggct	aggaacaatg	tgttgattca	cctcaaactc	300
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gcatggactg	ccgaagagaa	tagacatggt	gaccttctca	ataagtacct	ttatttgtct	600
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<212> PRT  
<213> Hedera helix

<220>  
<221> UNSURE  
<222> (318)

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Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
          35          40          45

Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
          50          55          60

Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
 65          70          75          80

Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
          85          90          95

Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
          100          105          110

Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
          115          120          125

Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
 130          135          140

Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
 145          150          155          160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
          165          170          175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
          180          185          190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
          195          200          205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
          210          215          220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
 225          230          235          240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
          245          250          255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
          260          265          270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
          275          280          285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
          290          295          300

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Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr  
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp  
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln  
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys  
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Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe  
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Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile  
385 390

<210> 3

<211> 445

<212> DNA

<213> Hedera helix

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catcgatttc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180  
gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240  
cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300  
ttgtgcggaa acaactggcg ctgccgctga ttctgcaagt cactggagag tcaaaattcg 360  
cagcgcttgg ggctgattct ctgcacacgg ttgagattgt gatgggacta aaggaggaaat 420  
tcggaatcaa gcgtgggaaa aagaa 445

<210> 4

<211> 114

<212> PRT

<213> Hedera helix

<400> 4

Met Ala Ser Val Thr Ala Ser Ser Ile Ser Phe Thr Ser Ile Ala Ser  
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20 25 30

Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu  
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val  
50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val  
65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
85 90 95

Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly  
100 105 110

Lys Lys  
114

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<211> 920  
<212> DNA  
<213> Hedera helix

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catcgatttc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180  
gttcaatttc actctctgtc aatgggaaat ccttccgttc acttaggttg ctgtcggcac 240  
cacttcgctt cagagtgtca tgcgcagcga aaccagcgac agtggacaag gtgtgtgaga 300  
ttgtgcggaa acaactggcg ctgccggctg attctgcagt cactggagag tcaaaattcg 360  
cagcgcttgg ggctgattct ctgcacacgg ttgagattgt gatgggacta gaggaggaat 420  
tcggaatcag cgtggaagaa gaaagtgcac agaccattgc cactgttcaa gatgcagcgg 480  
acctgattga gaagcttgtt gagaaaaagg agtagaagaa ccggggtaga aattctgcaa 540  
aataggttta ttaaggacag ttactttatt aggatggttc atcaagatct tcattaccct 600  
acatttatct gtatgctcct catgaagccg caaaagtagt agtggtgatg aaatttacc 660  
cgagtcttcg ccttaattat caaagtgaga gagccagaaa aagaggctat gctatctctc 720  
atctcgttat gttttatctt cttgtcggac ttctgggttg agtttttttt ttttatctaa 780  
acatgatatt agtcttgttt aaaagtttct caaaaaaata tatcttggtg ttgagactga 840  
tgtagattatt gctcttgata ttttgaatgt attttgagtt attcaaaaaa aaaaaaaaaa 900  
aaaaaaaaaa aaaaaaaaaa 920

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<212> PRT  
<213> Hedera helix

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Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu  
35 40 45  
Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val  
50 55 60  
Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val  
65 70 75 80  
Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
85 90 95  
Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu  
100 105 110  
Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gln Asp Ala Ala Asp Leu  
115 120 125  
Ile Glu Lys Leu Val Glu Lys Lys Glu  
130 135

# 2025-2026

5

His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr  
 290 295 300  
 Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp  
 305 310 315 320  
 Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly  
 325 330 335  
 Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala  
 340 345 350  
 Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys  
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 Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile  
 370 375 380

Ile  
385

<210> 8  
 <211> 137  
 <212> PRT  
 <213> Coriandrum sativum

<400> 8  
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 Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu  
 35 40 45  
 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Glu Thr Val Glu Lys Val  
 50 55 60  
 Cys Glu Ile Val Lys Lys Gln Leu Ala Leu Pro Pro Thr Thr Glu Val  
 65 70 75 80  
 Ser Gly Asp Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr  
 85 90 95  
 Val Glu Ile Val Met Gly Leu Glu Glu Glu Phe Gly Ile Ser Val Glu  
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 115 120 125  
 Ile Glu Lys Leu Cys Glu Lys Lys Glu  
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<210> 9  
 <211> 1381  
 <212> DNA  
 <213> Hedera helix



Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp  
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 Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp  
 165 170 175  
 Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys  
 180 185 190  
 Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys  
 195 200 205  
 Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu  
 210 215 220  
 Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His  
 225 230 235 240  
 Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp  
 245 250 255  
 Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala  
 260 265 270  
 Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg  
 275 280 285  
 Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu  
 290 295 300  
 Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Gly Val Tyr  
 305 310 315 320  
 Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp  
 325 330 335  
 Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln  
 340 345 350  
 Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys  
 355 360 365  
 Val Gln Gly Lys Glu Lys Lys Lys Lys Ala Glu His Pro Val Ser Phe  
 370 375 380  
 Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile  
 385 390

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 11

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<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> PCR primer  
  
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27

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